EXHIBIT E: Mouse FucT-VII gene, from phage 104, annotated with DNA sequencing primers used to sequence the phage, with start and stop codons, and with relevant restriction sites. Mouse genomic DNA sequence displayed from position 25,277,900 to 25,282,400 containing the coding sequence for the mouse FucT-VII gene

	CTGGTTGGAC GACCAACCTG					60
	ATCCTGGAAC TAGGACCTTG					120
	GAGGTGAGGT CTCCACTCCA					180
	CCCCCCACCC GGGGGGTGGG					240
	CAGTTGGCAA GTCAACCGTT					300
	CCAAACTGAG GGTTTGACTC					360
	TCCTTCAAAT AGGAAGTTTA					420
	CCCCAGCCAG GGGGTCGGTC					480
CAGAAGCCTG	TGGCCCCAAG ACCGGGGTTC	CTGGCAGGAT	GGCCCCCTTC	PstI CTGCAGGTCC	CCCACAGCCT	540
TCTGGGTTCC	TGACACGAGA ACTGTGCTCT	GAAGAGGTGG	GGCGGGGTGA	AGTGAACTCT	GAAGCCAAAA	600
TGTGACTCTC	CTGGGGTCAC	CAGCTTGGGG	AGAGGTGAAG	AAAGATGCCG	GGGCGGAAAC	660
E	GACCCCAGTG CORI ATATCACTAT				1088B	720
	TATAGTGATA CACCTCGTGC			9392A		780
ATGGCGACGG	GTGGAGCACG TACCCTCCCT	GGTGGAATGC	AATATGGAGT	TTGGTCGATC	TATCAAAGAC	
TACCGTGGGT	ATGGGAGGGA 1042B	AGGGGAAATC 8660B	CGTAACGCGT	TCGAGAGGTG	GTGTTAGACC	
TTCAATATGG	CTGCGAGGGG GACGCTCCCC	TACCCGTCCC	GTGAAGACTC	CACGGTTACT	CGGACGTGAT 9393A	
	TGGCCATGGC ACCGGTACCG					960
	GACTATGGCT CTGATACCGA 986B					1020
	TCGGGTCGGG AGCCCAGCCC	CAGAGCGAAG				1080
	GCCAACACTG CGGTTGTGAC			AGTCTGGAGC		1140

EXHIBIT E

GGACAAGCCA GGCCTGCTAT CCTGTTCGGT CCGGACGATA					1200
GGGGATCTGG TGGGGATGGA CCCCTAGACC ACCCCTACCT					1260
GTGACCCTGC TGGGCCACCC CACTGGGACG ACCCGGTGGC					1320
AGGCTTGGTG AGATGGAGAC TCCGAACCAC TCTACCTCTC					1380
GCTGGAGGGG AATCAAACAA	GCCTGGACCT		CTAGCTTTCC		1440
Start codon GTGGATGCCA ACCCCCTGCC CACCTACGGT TGGGGGACGC	CACCAGCCTG	CCTGTCCACG	CCAGGGACAC	ACAGAC TCCT	946B 1500
TCCCTTTCCA GACTGGAAAC AGGGAAAGGT CTGACCTTTC 715B 2931B					1560
TTCCAGCCCT GGACCTTGGC AAGGTCGGGA CCTGGAACCC					1620
GCAGGGAAAG ATAAGAATCC CGTCCCTTTC TATTCTTAGC		CTCCCCCCCG		CACTGCAGGT	1680
AGCTCCTGGG TCTGCCCTTC					1740
TTTTCTGAGG ATGACAATTC		GCATTTTCT			1800
TTGTGATGCC CGAGGATCTC AACACTACGG GCT CCTAGA C	CCTCGTGTCC				1860
GTATCATCAT TACAGGGAGG CATAGTAGTA ATGTCCCTCC	GGCCTCTGTG	GCCTCCTGGG			1920
GGGTGGCCTG GGGTTGTGTC CCCACCGGAC CCCAACACA					1980
CTTCTGCTCA GAGTGCTCGC GAAGACGAGT CTCACGAGCC					2040
TCCTCCTCTT CCTCCTTCTC AGGAGGAGAA GGAGGAAGAC					2100

EXHIBIT E

					8953	
			TGTCTTGGCC ACAGAACCGG		CTCAATTCCC GAGTTAAGGG	2160
			AGGGTTGGAT TCCCAACCTA 3512B		GCCAAAGATT CGGTTTCTAA	2220
				TCCTCACCTT	GGTAGATGGT CCATCTACCA	2280
			GCTGTGATTT CGACACTAAA 8904		CTGTTGGAGA GACAACCTCT	2340
					TCCAGATGAA AGGTCTACTT	2400
	CTCACGGACC	CCCTTAAGCA	GTCCCAGCTG CAGGGTCGAC 8902		GGATTTATGG CCTAAATACC KpnI	2460
	GCCTAGGGTG	ACAGGGCCTC			TTCAGGGTAC	2520
			GGCCTAGCTG CCGGATCGAC		ATTCATGGTA TAAGTACCAT	2580
			CCTGGAAGTG GGACCTTCAC		TCAGTCCACA AGTCAGGTGT	2640
CTCACCATCC	TTATCTGGCA		ACCAACCGGC TGGTTGGCCG		ACCTGGTGAC TGGACCACTG	2700
ACCTGCACTC			CGTCTGAGTG GCAGACTCAC		CCTGCTAGCC GGACGATCGG 8867	2760
			GAGCTGCAAA CTCGACGTTT		TCTCCTACCC	2820
		ACAGCCTTGG	GTCTGGGCCT CAGACCCGGA		GCCCAGTAAT CGGGTCATTA	2880
			TTCAACTGGG AAGTTGACCC		TCGGCGTGAT AGCCGCACTA	2940
TCAGATATCT			GAGCCTCTCT CTCGGAGAGA		ATCCCCACTA TAGGGGTGAT	3000
			ATCAGCAATT TAGTCGTTAA PstI		GCAGCAGCGT CGTCGTCGCA 8852	3060
					TCGCGCCAGC	3120
		AACAGACGAC	CCCACTTTGG GGGTGAAACC		CTTCTACCTG GAAGATGGAC	3180
			ATCACTGAGA TAGTGACTCT	TCAAGACCGC	CAATGCCCTG GTTACGGGAC 3715	3240
			CCTCCTCGGG GGAGGAGCCC	CCACCTACGA	GGCTTTTGTG	3300
CCACCAGATG			TTCAGCTCTG AAGTCGAGAC	CCCGTGAACT	GGCTGTCTTC CCGACAGAAG	3360

EXHIBIT E

TGAATGAGAG ACTTACTCTC 886	AGCAATAGCA	CCGAAGAAAC		CCGGCTCCGT GGCCGAGGCA	3420
TGGGTGACTG ACCCACTGAC			AGACACGGGC		
GCCAGGTCTA CGGTCCAGAT			TCCAGGCTTG		8876 3540
GCTGGATGGG CGACCTACCC			CAAAGAGCTG GTTTCTCGAC	GGCATCCAGG	3600
GGTACCGTCA				GAATTCAGGA CTTAAGTCCT	3660
	GAGATGCCCT			CCCAGGATAA GGGTCCTATT	3720
ATTAATGAGG TAATTACTCC				GACTTACCTT CTGAATGGAA	3780
TGAAGGCTCC ACTTCCGAGG 895	TACGGGTACC			TTCTATAGTC AAGATATCAG	3840
	TGCAGATGCA		GAGACCCACG	AGACTGTACA TCTGACATGT	3900
GGGGTTGTGG CCCCAACACC		CAGATGATTC GTCTACTAAG	TGGGCTTTTG ACCCGAAAAC	ACACCACAGT TGTGGTGTCA d and under	
AAAGAGGCAC TTTCTCCGTG SacI		AACACTGACA	GAAATCTCCT	GGTCAAGTCT	
				CAGCCATTAT GTCGGTAATA	4080
GTTTCTGTCT CAAAGACAGA				GAACTCAAAG CTTGAGTTTC	4140
GTACAGACCT CATGTCTGGA				AGGTGCCACA TCCACGGTGT	4200
CTCAGTGGGA GAGTCACCCT Ps:	CCACACAGGA			TCCGTTAGGG AGGCAATCCC	4260
	GCAGGTGCCC			CCAGGAGGAG GGTCCTCCTC	4320
AGGCTATGAG TCCGATACTC				TGGGGCTTGG ACCCCGAACC	4380
GGATGGGGTG CCTACCCCAC				GTGGTTTGTG CACCAAACAC	4440
AACCATGGCT TTGGTACCGA					4485